Algal Genomics

7A.1

NATURE, NURTURE AND THE STRUCTURE OF MACROALGAL GENOMES

J. Mark Cock[1,2] (cock@sb-roscoff.fr), Jonas Collén[1,2], Lieven Sterck[3,4], Pierre Rouzé[3,4], Delphine Scornet[1,2], Veronique Anthouard[5], François Artiguenave[5], Jean-Marc Aury[5], Kenny Billiau[3,4], Eric Bonnet[3,4], John H.F. Bothwell[6,7,8], Loraine Brillet[9], Wilfrid Carre[9], Susana M. Coelho[1,2], Erwan Corre[9], Corinne Da Silva[5], Claire Jubin[5], Cindy Martens[3,4], Florian Maumus[10], Diego Miranda-Saavedra[11], Akira F. Peters[1,2], Betina Porcel[5], Hadi Quesneville[12], Catherine Boyen[1,2], Yves Van de Peer[3,4] and Patrick Wincker[5]

[1]UPMC Univ. Paris 06, The Marine Plants and Biomolecules Laboratory, UMR 7139, Station Biologique de Roscoff, Place Georges Teissier, BP74, 29682 Roscoff Cedex, France; [2]CNRS, UMR 7139, Laboratoire International Associé Dispersal and Adaptation in Marine Species, Station Biologique de Roscoff, Place Georges Teissier, BP74, 29682 Roscoff Cedex, France; [3]Department of Plant Systems Biology, VIB, B-9052 Ghent, Belgium; [4]Department of Plant Biotechnology and Genetics, Ghent University, B-9052 Ghent, Belgium; [5]CEA, DSV, Institut de Génomique, Génoscope, 2 rue Gaston Crémieux, CP5706, 91057 Evry, France; [6]Queen's University Belfast, School of Biological Sciences, 97 Lisburn Road, Belfast, BT9 7BL, UK; [7]Queen's University Marine Laboratory, Portaferry, Co. Down, BT22 1PF, UK; [8]Marine Biological Association of the UK, The Laboratory, Citadel Hill, Plymouth, PL1 2PB, UK; [9]Computer and Genomics Resource Centre, FR 2424, Station Biologique de Roscoff, Place Georges Teissier, BP74, 29682 Roscoff Cedex, France; [10]Institut de Biologie de l'Ecole Normale Supérieure (IBENS), Centre National de la Recherche Scientifique UMR8197, Ecole Normale Supérieure, 75005 Paris, France; [11]Department of Haematology, Cambridge Institute for Medical Research, University of Cambridge, Hills Road, Cambridge CB2 0XY, UK and [12]Unité de Recherches en Génomique-Info (UR INRA 1164), INRA, Centre de recherche de Versailles, bat.18, RD10, Route de Saint Cyr, 78026 Versailles Cedex, France

The recent acquisition and analysis of complete genome sequences for two macroalgal species has provided unparalleled insights into the biology and evolutionary history of these important organisms. The recently published genome sequence of the filamentous brown alga *Ectocarpus siliculosus* (Cock *et al.*, Nature 2010) has not only provided clues as to how brown alga have adapted to the harsh conditions of the intertidal, but has also allowed the generation of hypotheses about the molecular events underlying the evolution of complex multicellular development in this group of organisms. The more recently completed genome sequence of the red alga *Chondrus crispus* (Collén *et al.*, unpublished) has similarly provided important information about the origins and the biology of the red algae. Both *Ectocarpus* and *Chondrus* are found in the intertidal zone, but they have had very different evolutionary histories and have been evolving independently for more than a billion years. Interestingly, they also exhibit very marked differences in terms of genome structure and organisation, suggesting that their evolutionary histories have played a more important role in shaping their genomes than their adaptation to the intertidal environment.